

SEQUENCE LISTING

<110> Bidney, Dennis
 Duvick, Jon
 Hendrick, Carol
 Hu, Xu
 Lu, Guihua
 Crasta, Oswald

<120> Sunflower RhoGAP, LOX, ADH and SCIP -
 Polynucleotides and Methods of Use

<130> 35718/201902

<150> US 60/166,128

<151> 1999-11-18

<150> US 60/201,837

<151> 2000-05-03

<160> 10

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 824

<212> DNA

<213> Helianthus annuus

<220>

<221> misc_feature

<222> (0)...(0)

<223> rhoGAP

<221> CDS

<222> (35)...(637)

<400> 1

ttcggcacga gtccaaatcc aatcttcaat cacc atg gct gaa gaa caa ctg ccg	55
Met Ala Glu Glu Gln Leu Pro	
1 5	
cct gat caa att aaa ctc att cac aag ctt aat ttg ttc aaa atc aaa	103
Pro Asp Gln Ile Lys Leu Ile His Lys Leu Asn Leu Phe Lys Ile Lys	
10 15 20	
ggc aga gat aaa cac aat cgc aaa atc tta cga att gtc gga aaa aac	151
Gly Arg Asp Lys His Asn Arg Lys Ile Leu Arg Ile Val Gly Lys Asn	
25 30 35	
ttt cca gct aag agt ttg acc gtt gac ctg ttg aaa aaa tat cta gaa	199
Phe Pro Ala Lys Ser Leu Thr Val Asp Leu Lys Lys Tyr Leu Glu	
40 45 50 55	
gtg aaa att ttc ccc aaa ctt gaa cga ccg ttt gtg gtg gtt tac gtt	247
Val Lys Ile Phe Pro Lys Leu Glu Arg Pro Phe Val Val Val Tyr Val	
60 65 70	
cac act gat gtt cag aag agc gag aat ttc cct gga ata tcc gtt ctc	295
His Thr Asp Val Gln Lys Ser Glu Asn Phe Pro Gly Ile Ser Val Leu	

75							80				85							
cgg	tca	gtt	tac	gac	gcg	att	cgg	atg	acc	gtg	aaa	caa	tat	ctt	gag	343		
Arg	Ser	Val	Tyr	Asp	Ala	Ile	Pro	Met	Thr	Val	Lys	Gln	Tyr	Leu	Glu			
90							95				100							
gcg	gtt	tac	ttt	gtt	cat	cgg	gat	ctg	cag	tcc	aga	att	ttt	ctg	gct	391		
Ala	Val	Tyr	Phe	Val	His	Pro	Asp	Leu	Gln	Ser	Arg	Ile	Phe	Leu	Ala			
105							110				115							
aca	ttt	ggc	cgg	ctt	atc	ttc	acc	gga	ggg	tta	tat	gca	aag	ctg	aga	439		
Thr	Phe	Gly	Arg	Leu	Ile	Phe	Thr	Gly	Gly	Leu	Tyr	Ala	Lys	Leu	Arg			
120							125				130				135			
ttt	gtg	agt	cga	ttg	gcg	tat	ctg	tgg	gaa	cat	gtg	aaa	agg	aac	gag	487		
Phe	Val	Ser	Arg	Leu	Ala	Tyr	Leu	Trp	Glu	His	Val	Lys	Arg	Asn	Glu			
140							145				150							
atc	gag	atc	cca	gag	ttt	gtc	tac	gat	cat	gat	gag	gat	ctg	gag	tac	535		
Ile	Glu	Ile	Pro	Glu	Phe	Val	Tyr	Asp	His	Asp	Glu	Asp	Leu	Glu	Tyr			
155							160				165							
cgt	cgg	atg	atg	gat	tac	ggg	ata	gag	agt	gac	cac	gct	aga	gtt	tat	583		
Arg	Pro	Met	Met	Asp	Tyr	Gly	Ile	Glu	Ser	Asp	His	Ala	Arg	Val	Tyr			
170							175				180							
gga	gcg	ccc	gcg	gtt	gat	tcc	tct	gtg	gcg	gct	tat	tcc	atg	agg	tgt	631		
Gly	Ala	Pro	Ala	Val	Asp	Ser	Ser	Val	Ala	Ala	Tyr	Ser	Met	Arg	Cys			
185							190				195							
atc	tca	tagggg	aaat	agttgt	tttt	tctttt	gttt	ttgaaa	atag	gtgcta	aaag					687		
Ile	Ser																	
200																		
aagt	gcaata	tatagt	tatt	agcaat	tatt	cgggtg	ttgt	agtatg	ttga	taacgg	gctt					747		
tctt	tataac	attcatt	gttt	ctagtt	tttct	tttgta	aaaaa	ttattt	tgata	aattct	ttgt					807		
aaaaaaaaa aaaaaaa																824		

```
<210> 2
<211> 201
<212> PRT
<213> Helianthus annuus
```

<400>	2																
Met	Ala	Glu	Glu	Gln	Leu	Pro	Pro	Asp	Gln	Ile	Lys	Leu	Ile	His	Lys		
1				5					10					15			
Leu	Asn	Leu	Phe	Lys	Ile	Lys	Gly	Arg	Asp	Lys	His	Asn	Arg	Lys	Ile		
			20					25					30				
Leu	Arg	Ile	Val	Gly	Lys	Asn	Phe	Pro	Ala	Lys	Ser	Leu	Thr	Val	Asp		
			35				40					45					
Leu	Leu	Lys	Lys	Tyr	Leu	Glu	Val	Lys	Ile	Phe	Pro	Lys	Leu	Glu	Arg		
						55					60						
Pro	Phe	Val	Val	Val	Tyr	Val	His	Thr	Asp	Val	Gln	Lys	Ser	Glu	Asn		
65					70					75					80		
Phe	Pro	Gly	Ile	Ser	Val	Leu	Arg	Ser	Val	Tyr	Asp	Ala	Ile	Pro	Met		
				85					90					95			
Thr	Val	Lys	Gln	Tyr	Leu	Glu	Ala	Val	Tyr	Phe	Val	His	Pro	Asp	Leu		
			100					105					110				
Gln	Ser	Arg	Ile	Phe	Leu	Ala	Thr	Phe	Gly	Arg	Leu	Ile	Phe	Thr	Gly		
			115				120					125					
Gly	Leu	Tyr	Ala	Lys	Leu	Arg	Phe	Val	Ser	Arg	Leu	Ala	Tyr	Leu	Trp		
			130			135					140						
Glu	His	Val	Lys	Arg	Asn	Glu	Ile	Glu	Ile	Pro	Glu	Phe	Val	Tyr	Asp		

145 150 155 160
 His Asp Glu Asp Leu Glu Tyr Arg Pro Met Met Asp Tyr Gly Ile Glu
 165 170 175
 Ser Asp His Ala Arg Val Tyr Gly Ala Pro Ala Val Asp Ser Ser Val
 180 185 190
 Ala Ala Tyr Ser Met Arg Cys Ile Ser
 195 200

<210> 3
 <211> 2943
 <212> DNA
 <213> Helianthus annuus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> lox cDNA

<221> CDS
 <222> (18)...(2720)

<400> 3
 ggcacgagaa gaaaacc atg ttg aat tct caa atc aac cat tct cac cct 50
 Met Leu Asn Ser Gln Ile Asn His Ser His Pro
 1 5 10
 ctt aac aac cta cta cca atc cgc aaa gcc ttt gtc cat ggt gac acc 98
 Leu Asn Asn Leu Leu Pro Ile Arg Lys Ala Phe Val His Gly Asp Thr
 15 20 25
 act aac cat tcc tcc tcc aac gcc tac tcc ccc gcc aac ctt cgc caa 146
 Thr Asn His Ser Ser Ser Asn Ala Tyr Ser Pro Ala Asn Leu Arg Gln
 30 35 40
 cac gcg tcc acc aag aaa tcc aat gct acc cgt gca cga tcc acc tca 194
 His Ala Ser Thr Lys Lys Ser Asn Ala Thr Arg Ala Arg Ser Thr Ser
 45 50 55
 act gcg ggt aac att aaa gcc ata tca atc ccc ttt ctt acc aag gag 242
 Thr Ala Gly Asn Ile Lys Ala Ile Ser Ile Pro Phe Leu Thr Lys Glu
 60 65 70 75
 acc acc gtc aag tgt gtc atc acc gtc caa cca acc att agt tcc gcc 290
 Thr Thr Val Lys Cys Val Ile Thr Val Gln Pro Thr Ile Ser Ser Ala
 80 85 90
 att gct ggt gta ggc gtt ggt ggt att gtt gat ggt gtt tct aat ctt 338
 Ile Ala Gly Val Gly Val Gly Gly Ile Val Asp Gly Val Ser Asn Leu
 95 100 105
 cta ggg ttg tca ttt ttg ttg gag ctc gtt tca aat gac ctc gat tca 386
 Leu Gly Leu Ser Phe Leu Leu Glu Leu Val Ser Asn Asp Leu Asp Ser
 110 115 120
 aaa gga aac caa aag aca gtg aag gct tat gca aga tac aac gca ctg 434
 Lys Gly Asn Gln Lys Thr Val Lys Ala Tyr Ala Arg Tyr Asn Ala Leu
 125 130 135
 gat ttg gac att agc gtg tac aca tac aaa tgc gac ttc gac gtc cct 482
 Asp Leu Asp Ile Ser Val Tyr Thr Tyr Lys Cys Asp Phe Asp Val Pro
 140 145 150 155
 gaa gat ttt ggg gag ata gga gct gtg ttg gta gaa aat gag tat agc 530

Glu Asp Phe Gly Glu Ile Gly Ala Val	Leu Val Glu Asn Glu Tyr Ser	
160	165	170
aag aag atg ttt ttc aag aac att gtt ctt aac aac ggt gtt acc ttc		578
Lys Lys Met Phe Phe Lys Asn Ile Val Leu Asn Asn Gly Val Thr Phe		
175	180	185
aca tgc gag tca tgg gtt cac tcc aaa tac gat aac cct gag aaa aga		626
Thr Cys Glu Ser Trp Val His Ser Lys Tyr Asp Asn Pro Glu Lys Arg		
190	195	200
ata ttt ttc acc gac aag tgc tat cta ccg ttg gaa acg ccg acg gca		674
Ile Phe Phe Thr Asp Lys Ser Tyr Leu Pro Leu Glu Thr Pro Thr Ala		
205	210	215
ctg aag ccg tta cga gag aaa gat atg gaa tgc ctt cga gga aac ggc		722
Leu Lys Pro Leu Arg Glu Lys Asp Met Glu Ser Leu Arg Gly Asn Gly		
220	225	230
gaa gga gaa cgt aaa tca ttc gag ccg ata tat gat tat gat gtg tac		770
Glu Gly Glu Arg Lys Ser Phe Glu Arg Ile Tyr Asp Tyr Asp Val Tyr		
240	245	250
aac gat ctc gga gat ccg gat gga agc tta gat cta gca ccg ccg gtg		818
Asn Asp Leu Gly Asp Pro Asp Gly Ser Leu Asp Leu Ala Arg Pro Val		
255	260	265
ctc ggt ggc gag aca cat ccg tac cct agg ccg tgc cgt act ggt cgc		866
Leu Gly Gly Glu Thr His Pro Tyr Pro Arg Arg Cys Arg Thr Gly Arg		
270	275	280
aaa atg tcc tct aaa gat ccg tta aca gaa agc aga act acg ctc cct		914
Lys Met Ser Ser Lys Asp Pro Leu Thr Glu Ser Arg Thr Thr Leu Pro		
285	290	295
ttt tat gta cct gcg gat gaa gat ttt tca gag ata aag agt gtg aac		962
Phe Tyr Val Pro Ala Asp Glu Asp Phe Ser Glu Ile Lys Ser Val Asn		
300	305	310
ttt gga gca aaa act tta tac tct gtg ctt cat gga gtt gta cca atg		1010
Phe Gly Ala Lys Thr Leu Tyr Ser Val Leu His Gly Val Val Pro Met		
320	325	330
cta gac tca att gta aca gac aaa gac aag ggg ttt cca tta ttc aca		1058
Leu Asp Ser Ile Val Thr Asp Lys Asp Lys Gly Phe Pro Leu Phe Thr		
335	340	345
tcc ata gat ttg ctt tat aat gaa ggt gtt aat gtt cct tct cct gac		1106
Ser Ile Asp Leu Leu Tyr Asn Glu Gly Val Asn Val Pro Ser Pro Asp		
350	355	360
aat gga att cta agt gct tta cct aga ctt gtc aaa ggg gct act gat		1154
Asn Gly Ile Leu Ser Ala Leu Pro Arg Leu Val Lys Gly Ala Thr Asp		
365	370	375
gcc gca aat acc gtt atc aag ttc gag acc ccc gaa acc att gat aga		1202
Ala Ala Asn Thr Val Ile Lys Phe Glu Thr Pro Glu Thr Ile Asp Arg		
380	385	390
gac gca ttc tca tgg ttc cgt gat gaa gag ttc tgc ccg caa atg ctt		1250
Asp Ala Phe Ser Trp Phe Arg Asp Glu Glu Phe Cys Arg Gln Met Leu		
400	405	410

gat tac cca tat gca aat gat ggt tta ctc att tat gat acc att aaa Asp Tyr Pro Tyr Ala Asn Asp Gly Leu Leu Ile Tyr Asp Thr Ile Lys	2066
670 675 680	
caa tgg gca act tct tat gtc aac cac tat tac cca cca gcg aat cta Gln Trp Ala Thr Ser Tyr Val Asn His Tyr Tyr Pro Pro Ala Asn Leu	2114
685 690 695	
gtg gaa tct gat gaa gag ctt caa gca tgg tgg aat gaa atc cgt aca Val Glu Ser Asp Glu Glu Leu Gln Ala Trp Trp Asn Glu Ile Arg Thr	2162
700 705 710 715	
gtt ggt cat gga gat aag aaa gat gaa cca tgg tgg cca caa ctc aaa Val Gly His Gly Asp Lys Lys Asp Glu Pro Trp Trp Pro Gln Leu Lys	2210
720 725 730	
acc caa gat gat ttg att gga att gtt tca acc atc ttg tgg gtg acc Thr Gln Asp Asp Leu Ile Gly Ile Val Ser Thr Ile Leu Trp Val Thr	2258
735 740 745	
tct ggt caa cat tca gca gtc aac ttc ggt caa tat gat ttc gcg ggt Ser Gly Gln His Ser Ala Val Asn Phe Gly Gln Tyr Asp Phe Ala Gly	2306
750 755 760	
tat ttc cct aac agg ccg aca att tcc aga acc aaa atg ccc aac gaa Tyr Phe Pro Asn Arg Pro Thr Ile Ser Arg Thr Lys Met Pro Asn Glu	2354
765 770 775	
gac ccc aca gac gaa gaa tgg cag tcg ttt ata aag cga ccc gag gat Asp Pro Thr Asp Glu Glu Trp Gln Ser Phe Ile Lys Arg Pro Glu Asp	2402
780 785 790 795	
gct tta ttg aaa tgc ttc cca tcc caa atc caa gct aca aaa gtg atg Ala Leu Leu Lys Cys Phe Pro Ser Gln Ile Gln Ala Thr Lys Val Met	2450
800 805 810	
gcg att ttg gat gtt tta tca agt cat tca cca gat gaa gaa tat atc Ala Ile Leu Asp Val Leu Ser Ser His Ser Pro Asp Glu Glu Tyr Ile	2498
815 820 825	
ggt gga aat att gag gcg gca tgg gag gcg gag cct gct ata aaa gca Gly Gly Asn Ile Glu Ala Ala Trp Glu Ala Glu Pro Ala Ile Lys Ala	2546
830 835 840	
gcc ttt gag gag ttc cgt gga agg ctc aat gag ctg gaa gca atc ata Ala Phe Glu Glu Phe Arg Gly Arg Leu Asn Glu Leu Glu Ala Ile Ile	2594
845 850 855	
gac tca agg aac acg gat ccc aat ttg aag aat cgt agt ggt gcg ggg Asp Ser Arg Asn Thr Asp Pro Asn Leu Lys Asn Arg Ser Gly Ala Gly	2642
860 865 870 875	
ttg gtt ccg tat caa ctt ctc aaa ccg tat tct gaa aaa ggt gtg acc Leu Val Pro Tyr Gln Leu Leu Lys Pro Tyr Ser Glu Lys Gly Val Thr	2690
880 885 890	
ggg aga ggt gtt cca aac agc ata tcc att tagttggatt ggtttggttc Gly Arg Gly Val Pro Asn Ser Ile Ser Ile	2740
895 900	
ctaagtctcg aggaatagtc tatgtggtgt aataaggcca tgatccatgg tttagtgtgtg ttttattgtt atttgaata agttcactta tgtgccttct tgtattataa gccaacatta	2800 2860

2943

<400> 4

[illegible]

Pro	Glu	Ile	Tyr	Gly	Pro	Ala	Glu	Ser	Ala	Ile	Thr	Lys	Glu	Ile	Val
	435						440					445			
Glu	Glu	Glu	Ile	Lys	Gly	Phe	Met	Thr	Leu	Glu	Glu	Ala	Leu	Ala	Gln
	450					455					460				
Lys	Lys	Leu	Phe	Met	Leu	Asp	Tyr	His	Asp	Leu	Leu	Leu	Pro	Tyr	Val
	465				470					475					480
Asn	Lys	Thr	Glu	Ala	Glu	Gly	Arg	Thr	Leu	Tyr	Gly	Ser	Arg	Thr	Leu
			485						490						495
Met	Phe	Leu	Thr	Pro	Ala	Gly	Thr	Leu	Arg	Pro	Leu	Ala	Ile	Glu	Leu
		500						505					510		
Thr	Arg	Pro	Pro	Ile	Asp	Gly	Lys	Pro	Gln	Trp	Lys	His	Val	Tyr	Thr
		515					520						525		
Pro	Ala	Trp	Asp	Ala	Thr	Gly	Ala	Trp	Leu	Trp	Lys	Leu	Ala	Lys	Ala
	530					535					540				
His	Val	Leu	Ala	His	Asp	Ser	Ser	Tyr	His	Gln	Leu	Val	Ser	His	Trp
	545				550					555					560
Leu	Arg	Thr	His	Cys	Ala	Thr	Glu	Pro	Tyr	Ile	Ile	Ala	Thr	Asn	Arg
				565					570						575
Gln	Leu	Ser	Gln	Met	His	Pro	Ile	Arg	Arg	Phe	Leu	Leu	Pro	His	Phe
		580						585					590		
Arg	Tyr	Thr	Met	Gln	Ile	Asn	Ser	Leu	Ala	Arg	Leu	Leu	Val	Asn	
		595					600					605			
Ala	Met	Gly	Ile	Ile	Glu	Ser	Thr	Phe	Ser	Pro	Gly	Arg	Tyr	Cys	Met
	610					615					620				
Gln	Ile	Ser	Ser	Asp	Ala	Tyr	Asp	Gln	Gln	Trp	Arg	Phe	Asp	His	Glu
	625				630					635					640
Ala	Leu	Pro	Ala	Asp	Leu	Ile	Ser	Arg	Gly	Met	Ala	Val	Glu	Asp	Pro
			645						650					655	
Thr	Ala	Pro	Tyr	Gly	Val	Lys	Leu	Thr	Ile	Glu	Asp	Tyr	Pro	Tyr	Ala
		660						665					670		
Asn	Asp	Gly	Leu	Leu	Ile	Tyr	Asp	Thr	Ile	Lys	Gln	Trp	Ala	Thr	Ser
		675					680						685		
Tyr	Val	Asn	His	Tyr	Tyr	Pro	Pro	Ala	Asn	Leu	Val	Glu	Ser	Asp	Glu
	690					695					700				
Glu	Leu	Gln	Ala	Trp	Trp	Asn	Glu	Ile	Arg	Thr	Val	Gly	His	Gly	Asp
	705				710					715					720
Lys	Lys	Asp	Glu	Pro	Trp	Trp	Pro	Gln	Leu	Lys	Thr	Gln	Asp	Asp	Leu
			725						730					735	
Ile	Gly	Ile	Val	Ser	Thr	Ile	Leu	Trp	Val	Thr	Ser	Gly	Gln	His	Ser
		740						745					750		
Ala	Val	Asn	Phe	Gly	Gln	Tyr	Asp	Phe	Ala	Gly	Tyr	Phe	Pro	Asn	Arg
		755					760					765			
Pro	Thr	Ile	Ser	Arg	Thr	Lys	Met	Pro	Asn	Glu	Asp	Pro	Thr	Asp	Glu
	770					775									

8

[illegible]

```
<221> misc_feature
<222> (322)...(327)
<223> W-box
```

```
<221> misc_feature
<222> (808)...(811)
<223> TATA box
```

```
<210> 6
<211> 1403
<212> DNA
<213> Helianthus annuus
```

<221> CDS
<222> (74) ... (1216)

9

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000

ttc act tcc ctc tgc cac act gat gtt tac ttc tgg gaa gcc aaa gga	253
Phe Thr Ser Leu Cys His Thr Asp Val Tyr Phe Trp Glu Ala Lys Gly	
45 50 55 60	
caa aat cct gta ttc cca aga att tta gga cat gaa gct gga ggg gtt	301
Gln Asn Pro Val Phe Pro Arg Ile Leu Gly His Glu Ala Gly Gly Val	
65 70 75	
gtg gag agt gtt ggg gaa gga gtg act gat ctt cag cca ggg gat cat	349
Val Glu Ser Val Gly Glu Gly Val Thr Asp Leu Gln Pro Gly Asp His	
80 85 90	
gtt ctt ccc gtt ttc acc gga gaa tgc aaa gag tgt gct cac tgt aag	397
Val Leu Pro Val Phe Thr Gly Glu Cys Lys Glu Cys Ala His Cys Lys	
95 100 105	
tcc gaa gag agc aac atg tgt gac ctt ctc agg atc aac acc gac agg	445
Ser Glu Glu Ser Asn Met Cys Asp Leu Leu Arg Ile Asn Thr Asp Arg	
110 115 120	
gga gtc atg ctt cac gat cag aaa tct cga ttc tcg atc aac ggc aaa	493
Gly Val Met Leu His Asp Gln Lys Ser Arg Phe Ser Ile Asn Gly Lys	
125 130 135 140	
ccc atc ttc cat ttt gtg ggg act tct act ttc agc gag tac acg gtt	541
Pro Ile Phe His Phe Val Gly Thr Ser Thr Phe Ser Glu Tyr Thr Val	
145 150 155	
gtt cat gtt gga tgt ctt gca aag atc aac cct ctt gcc cct ctt gat	589
Val His Val Gly Cys Leu Ala Lys Ile Asn Pro Leu Ala Pro Leu Asp	
160 165 170	
aaa gtt tgt gtt ctc agc tgt ggg atc tcc aca ggg ctg ggt gct act	637
Lys Val Cys Val Leu Ser Cys Gly Ile Ser Thr Gly Leu Gly Ala Thr	
175 180 185	
ttg aat gtt gca aaa ccg aaa aaa ggc tct tcg gtg gcg gtt ttc ggt	685
Leu Asn Val Ala Lys Pro Lys Lys Gly Ser Ser Val Ala Val Phe Gly	
190 195 200	
ctg ggg gca gtg gga ctt gct gct gct gaa ggt gca aga att tct ggg	733
Leu Gly Ala Val Gly Leu Ala Ala Ala Glu Gly Ala Arg Ile Ser Gly	
205 210 215 220	
gct tca aga atc att ggt gtt gat ctc aat gcc aat aga ttc gag ctt	781
Ala Ser Arg Ile Ile Gly Val Asp Leu Asn Ala Asn Arg Phe Glu Leu	
225 230 235	
gca aag aaa ttt ggg gtt aca gag ttt gtg aac cca aaa gat tat aag	829
Ala Lys Lys Phe Gly Val Thr Glu Phe Val Asn Pro Lys Asp Tyr Lys	
240 245 250	
aag ccg gtg caa gaa gtg att gca gag atg aca aat gga gga gtt gac	877
Lys Pro Val Gln Glu Val Ile Ala Glu Met Thr Asn Gly Gly Val Asp	
255 260 265	
agg agt gtt gaa tgc act ggt cat att gat gct atg atc tct gct ttt	925
Arg Ser Val Glu Cys Thr Gly His Ile Asp Ala Met Ile Ser Ala Phe	
270 275 280	
gaa tgt gtt cat gat ggg tgg ggt gtt gct gtt cta gta ggt gtt ccg	973
Glu Cys Val His Asp Gly Trp Gly Val Ala Val Leu Val Gly Val Pro	

	290	295	300	
285				1021
	cat aaa gat gcc gtg ttc aag acc agt ccc atg aat ctg ttg aac gaa His Lys Asp Ala Val Phe Lys Thr Ser Pro Met Asn Leu Leu Asn Glu		315	
	305	310		
	agg act ctg aag ggt acc ttc ttt gga aac tat aaa ccg cga tct gat Arg Thr Leu Lys Gly Thr Phe Phe Gly Asn Tyr Lys Pro Arg Ser Asp		330	1069
	320	325		
	att cct tcg gtt gtc gaa aag tat atg aac aag gaa ctt gag gtg gag Ile Pro Ser Val Val Glu Lys Tyr Met Asn Lys Glu Leu Glu Val Glu		345	1117
	335	340		
	aag ttc ata aca cat gaa gtg cca ttt tca gag atc aat aag ccc ttt Lys Phe Ile Thr His Glu Val Pro Phe Ser Glu Ile Asn Lys Pro Phe		360	1165
	350	355		
	gac ttg atg ctt aaa ggt gaa ggt ctt cgt tgc att att cga atg gat Asp Leu Met Leu Lys Gly Glu Gly Leu Arg Cys Ile Ile Arg Met Asp		375	1213
	365	370		
	gcc taaataattt caaactgtgc aagagagagc agtaggagtc gtctattcgt Ala			1266

A1a

aaagatatat	gtgtgtgttc	tcgtctctca	tcgtcgtaaa	tgtgtcctta	agatcttggt	1326
ttgttaattg	ttacccataa	aagattttga	atttgaataa	caatagaaat	tgatgtctaa	1386
aaaaaaaaaa	aaaaaaaa					1403

<400> 7

Met	Ser	Ser	Thr	Thr	Thr	Gly	Gln	Val	Ile	Arg	Cys	Lys	Ala	Ala	Val
1				5				10						15	
Thr	Trp	Glu	Ala	Gly	Lys	Pro	Leu	Val	Ile	Glu	Glu	Val	Glu	Val	Ala
		20						25					30		
Pro	Pro	Gln	Lys	Met	Glu	Val	Arg	Ile	Lys	Ile	Leu	Phe	Thr	Ser	Leu
		35				40						45			
Cys	His	Thr	Asp	Val	Tyr	Phe	Trp	Glu	Ala	Lys	Gly	Gln	Asn	Pro	Val
	50					55					60				
Phe	Pro	Arg	Ile	Leu	Gly	His	Glu	Ala	Gly	Gly	Val	Val	Glu	Ser	Val
65					70					75					80
Gly	Glu	Gly	Val	Thr	Asp	Leu	Gln	Pro	Gly	Asp	His	Val	Leu	Pro	Val
				85					90					95	
Phe	Thr	Gly	Glu	Cys	Lys	Glu	Cys	Ala	His	Cys	Lys	Ser	Glu	Glu	Ser
				100				105					110		
Asn	Met	Cys	Asp	Leu	Leu	Arg	Ile	Asn	Thr	Asp	Arg	Gly	Val	Met	Leu
		115					120					125			
His	Asp	Gln	Lys	Ser	Arg	Phe	Ser	Ile	Asn	Gly	Lys	Pro	Ile	Phe	His
	130					135					140				
Phe	Val	Gly	Thr	Ser	Thr	Phe	Ser	Glu	Tyr	Thr	Val	Val	His	Val	Gly
145					150					155					160
Cys	Leu	Ala	Lys	Ile	Asn	Pro	Leu	Ala	Pro	Leu	Asp	Lys	Val	Cys	Val
				165					170					175	
Leu	Ser	Cys	Gly	Ile	Ser	Thr	Gly	Leu	Gly	Ala	Thr	Leu	Asn	Val	Ala
				180				185					190		
Lys	Pro	Lys	Lys	Gly	Ser	Ser	Val	Ala	Val	Phe	Gly	Leu	Gly	Ala	Val
		195					200					205			
Gly	Leu	Ala	Ala	Ala	Glu	Gly	Ala	Arg	Ile	Ser	Gly	Ala	Ser	Arg	Ile

210 215 220
 Ile Gly Val Asp Leu Asn Ala Asn Arg Phe Glu Leu Ala Lys Lys Phe
 225 230 235 240
 Gly Val Thr Glu Phe Val Asn Pro Lys Asp Tyr Lys Lys Pro Val Gln
 245 250 255
 Glu Val Ile Ala Glu Met Thr Asn Gly Gly Val Asp Arg Ser Val Glu
 260 265 270
 Cys Thr Gly His Ile Asp Ala Met Ile Ser Ala Phe Glu Cys Val His
 275 280 285
 Asp Gly Trp Gly Val Ala Val Leu Val Gly Val Pro His Lys Asp Ala
 290 295 300
 Val Phe Lys Thr Ser Pro Met Asn Leu Leu Asn Glu Arg Thr Leu Lys
 305 310 315 320
 Gly Thr Phe Phe Gly Asn Tyr Lys Pro Arg Ser Asp Ile Pro Ser Val
 325 330 335
 Val Glu Lys Tyr Met Asn Lys Glu Leu Glu Val Glu Lys Phe Ile Thr
 340 345 350
 His Glu Val Pro Phe Ser Glu Ile Asn Lys Pro Phe Asp Leu Met Leu
 355 360 365
 Lys Gly Glu Gly Leu Arg Cys Ile Ile Arg Met Asp Ala
 370 375 380

<210> 8
 <211> 747
 <212> DNA
 <213> Helianthus annuus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> SCIP-1 cDNA

<221> CDS
 <222> (15)...(518)

<400> 8
 ttcggcacga gcaa atg gcg aac gca agc gat gag ttc aga cta gcg tct
 Met Ala Asn Ala Ser Asp Glu Phe Arg Leu Ala Ser
 1 5 10

tcc ggc atc gat cat gaa ggc cga cta cca cga aaa tac acc ggt gac
 Ser Gly Ile Asp His Glu Gly Arg Leu Pro Arg Lys Tyr Thr Gly Asp
 15 20 25

ggt caa ggt aca aaa aaa gac ata tca cca ccg tta gaa tgg tac aac
 Gly Gln Gly Thr Lys Lys Asp Ile Ser Pro Pro Leu Glu Trp Tyr Asn
 30 35 40

gtt ccg gag ggg aca aaa aca cta gca cta gtg gtg gag gac atc gat
 Val Pro Glu Gly Thr Lys Thr Leu Ala Leu Val Val Glu Asp Ile Asp
 45 50 55 60

gca ccg gac cca gaa gcg ccg ctg gtt ccg tgg act gtg tgg gtg gtg
 Ala Pro Asp Pro Glu Ala Pro Leu Val Pro Trp Thr Val Trp Val Val
 65 70 75

gtc aat ata cca cct act ttg aag ggg ctc cca gag gga ttt tcc ggg
 Val Asn Ile Pro Pro Thr Leu Lys Gly Leu Pro Glu Gly Phe Ser Gly
 80 85 90

aaa gag ggg gac atg ggt ggc gat tat gct aat gtt aaa gaa gga cat
 Lys Glu Gly Asp Met Gly Gly Asp Tyr Ala Asn Val Lys Glu Gly His
 95 100 105

50

98

146

194

242

290

338

aat gac ttt aag gtg cct gga tgg cgc gca ccg aag atg ccc tca tcc 386
 Asn Asp Phe Lys Val Pro Gly Trp Arg Ala Pro Lys Met Pro Ser Ser
 110 115 120
 gga cac cgg ttc gag ttt aag ctg tat gcg ttg gat gaa caa gtt gag 434
 Gly His Arg Phe Glu Phe Lys Leu Tyr Ala Leu Asp Glu Gln Val Glu
 125 130 135 140
 ttg ggg aat aag gtg act aag gag aag ttg ctg gag gcg att gat ggc 482
 Leu Gly Asn Lys Val Thr Lys Glu Lys Leu Leu Glu Ala Ile Asp Gly
 145 150 155
 cat gtg gtt ggg gag gct gtt ctg atg gcc gta aat taaattgaga 528
 His Val Val Gly Glu Ala Val Leu Met Ala Val Asn
 160 165
 atggtttata tatatgttag ttgtgtgact tgtgtcatgt gtgatgttct tgttttaacg 588
 tattttgaaa cagaagtgc gagagagaga gagggtttgt tgtgtgtttt tcttgagaga 648
 tcgtgaatta attatgctgt ttgtgttcaa ggaatcaagc ttataaaagt aaaatacaaa 708
 tgaatgctt caaccgagct aaaaaaaaaa aaaaaaaaaa 747

<210> 9
 <211> 168
 <212> PRT
 <213> Helianthus annus SCIP-1

<400> 9
 Met Ala Asn Ala Ser Asp Glu Phe Arg Leu Ala Ser Ser Gly Ile Asp
 1 5 10 15
 His Glu Gly Arg Leu Pro Arg Lys Tyr Thr Gly Asp Gly Gln Gly Thr
 20 25 30
 Lys Lys Asp Ile Ser Pro Pro Leu Glu Trp Tyr Asn Val Pro Glu Gly
 35 40 45
 Thr Lys Thr Leu Ala Leu Val Val Glu Asp Ile Asp Ala Pro Asp Pro
 50 55 60
 Glu Ala Pro Leu Val Pro Trp Thr Val Trp Val Val Asn Ile Pro
 65 70 75 80
 Pro Thr Leu Lys Gly Leu Pro Glu Gly Phe Ser Gly Lys Glu Gly Asp
 85 90 95
 Met Gly Gly Asp Tyr Ala Asn Val Lys Glu Gly His Asn Asp Phe Lys
 100 105 110
 Val Pro Gly Trp Arg Ala Pro Lys Met Pro Ser Ser Gly His Arg Phe
 115 120 125
 Glu Phe Lys Leu Tyr Ala Leu Asp Glu Gln Val Glu Leu Gly Asn Lys
 130 135 140
 Val Thr Lys Glu Lys Leu Leu Glu Ala Ile Asp Gly His Val Val Gly
 145 150 155 160
 Glu Ala Val Leu Met Ala Val Asn
 165

<210> 10
 <211> 513
 <212> DNA
 <213> Helianthus annus

<220>
 <221> promoter
 <222> (1)...(510)
 <223> SCIP promoter

<221> misc_feature
 <222> (364)...(368)

<223> W-box

<221> misc_feature

<222> (371)...(375)

<223> W-box

<221> misc_feature

<222> (415)...(420)

<223> G-box

<400> 10

cttccctatt	ttcggtaaca	cttgtgcggc	aaaggggttg	gcagtgggta	ccgctcggtg	60
ccgaaccact	ttgccgctgc	cactccgggc	agcctaaata	atgctatata	tgtgacattt	120
ttgcactgaa	ttctactttt	tatttaccat	acgcgatgaa	aaggcattgg	ttttttatta	180
tattatattt	cagtttctat	tttggacgg	caaaaatgaa	ttttattaaa	agtaaacgaa	240
tttaaaaata	ttcggataat	tactttttct	tttgaatctt	gattcggata	agttgttacg	300
aattttaaaa	cgacaattga	ttgaaaatga	gtgatgtagc	tctttctagc	gtaccacgta	360
tctgtcaagt	gtcaacatgc	tacagcttct	caaaactgct	agaactctta	actacacgtg	420
tccacaaacc	cacaaaatcc	taaccatcca	taacactata	agaacttgat	caacagatct	480
gttttagtaac	aagttattga	aggtacaaca	atg			513

CGTATTTTCTTCTATTTTGGACGGCAAAAATGAATTTTATTAAAGTAAACGAAAGTTGTACG